

Mailbox Room 12E12

U.S. DEPARTMENT OF COMMERCE  
Patent and Trademark Office

Office Room 12D07

## SEARCH REQUEST FORM

Requestor's

Name: Anne-Marie Baker

Serial

Number: 08/963,288Date: 8/15/02Phone: 306-9155Art Unit: 1632

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please search: nucleic acid databases for

TTCTGA GAA

I would like the search to be size-limited to less than 30 nucleotides (in other words, I don't want any hits for sequences over 30 nucleotides).

Note: The sequence is smaller than 10 nucleotides and therefore is not subject to compliance with the sequence rules.

Point of Contact:  
Barb O'Brien  
Technical Information Specialist  
STIC CM1 6A05 308-4291

## STAFF USE ONLY

Date completed: 8-21-02Searcher: BCBTerminal time: 12Elapsed time: prep 2576

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: \_\_\_\_\_

Search Site

\_\_\_\_ STIC

\_\_\_\_ CM-1

\_\_\_\_ Pre-S

Type of Search

\_\_\_\_ 1 N.A. Sequence

\_\_\_\_ A.A. Sequence

\_\_\_\_ Structure

\_\_\_\_ Bibliographic

Vendors

X IG

\_\_\_\_ STN

\_\_\_\_ Dialog

\_\_\_\_ APS

\_\_\_\_ Geninfo

\_\_\_\_ SDC

\_\_\_\_ DARC/Questel

abs 06 Other

**THIS PAGE BLANK (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 21:33:29 ; Search time 1861.18 Seconds  
(without alignments)  
101.193 Million cell updates/sec

Title: NA\_SEQ  
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 524256

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_da:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Length	DB ID	Description
-----				

C	1	9	100.0	15	6	AR133394	AR133394 Sequence
C	2	9	100.0	15	6	AR133395	AR133395 Sequence
C	3	9	100.0	18	6	AX277553	AX277553 Sequence
C	4	9	100.0	19	6	AR043730	AR043730 Sequence
C	5	9	100.0	19	6	AR043731	AR043731 Sequence
C	6	9	100.0	19	6	AX130312	AX130312 Sequence
C	7	9	100.0	19	6	I81958	I81958 Sequence
C	8	9	100.0	19	6	I81959	I81959 Sequence
C	9	9	100.0	20	6	A67540	A67540 Sequence
C	10	9	100.0	20	6	AR029053	AR029053 Sequence
C	11	9	100.0	20	6	AR120696	AR120696 Sequence
C	12	9	100.0	20	6	E03365	E03365 Sequence
C	13	9	100.0	22	6	AR040919	AR040919 Sequence
C	14	9	100.0	22	6	AR051826	AR051826 Sequence
C	15	9	100.0	22	6	AR115962	AR115962 Sequence
C	16	9	100.0	22	6	AR127329	AR127329 Sequence
C	17	9	100.0	22	6	AR168643	AR168643 Sequence
C	18	9	100.0	22	6	AR170236	AR170236 Sequence
C	19	9	100.0	22	6	AR171665	AR171665 Sequence
C	20	9	100.0	22	6	BD011555	BD011555 DNA mutag
C	21	9	100.0	22	6	I36216	I36216 Sequence
C	22	9	100.0	23	6	AR097057	AR097057 Sequence
C	23	9	100.0	23	6	E36223	E36223 Japanese cl
C	24	9	100.0	23	6	E47019	E47019 Simulaneol
C	25	9	100.0	24	6	A02218	A02218 Oligonucleo
C	26	9	100.0	24	6	A81021	A81021 Sequence
C	27	9	100.0	24	6	AR036118	AR036118 Sequence
C	28	9	100.0	24	6	AR136874	AR136874 Sequence
C	29	9	100.0	24	6	AX008844	AX008844 Sequence
C	30	9	100.0	24	6	AX008851	AX008851 Sequence
C	31	9	100.0	24	6	AX008852	AX008852 Sequence
C	32	9	100.0	24	6	E25644	E25644 Novel phes
C	33	9	100.0	25	6	A98319	A98319 Sequence
C	34	9	100.0	25	6	AR104820	AR104820 Sequence
C	35	9	100.0	25	6	AX027405	AX027405 Sequence
C	36	9	100.0	26	6	A59559	A59559 Sequence
C	37	9	100.0	26	6	AR116909	AR116909 Sequence
C	38	9	100.0	26	6	AR128122	AR128122 Sequence
C	39	9	100.0	26	6	AR170508	AR170508 Sequence
C	40	9	100.0	26	6	AX080772	AX080772 Sequence
C	41	9	100.0	26	6	AX107138	AX107138 Sequence
C	42	9	100.0	26	6	AX201406	AX201406 Sequence
C	43	9	100.0	26	6	I04554	I04554 Sequence
C	44	9	100.0	26	6	I46574	I46574 Sequence
C	45	9	100.0	26	6	I46579	I46579 Sequence

## ALIGNMENTS

RESULT	1	15 bp	DNA	linear	PAT	16-MAY-2001
AR133394/c	Sequence 1819 from patent US 6194150.					
LOCUS	AR133394					
DEFINITION	Sequence 1819 from patent US 6194150.					
ACCESSION	AR133394					
VERSION	AR133394.1	GI:14122299				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 15)					
AUTHORS	Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.					
TITLE	Nucleic acid based inhibition of CD40					
JOURNAL	Patent: US 6194150-A 1819 27-FEB-2001;					
FEATURES	location/Qualifiers					
source	1..15					
BASE COUNT	5 a 3 c 3 g 4 t					
ORIGIN	1..15					

Query Match 100.0%; Score 9; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9  
 |||||  
 DB 15 TTCTGAGAA 7

RESULT 2  
 ARI33395/C ARI33395 15 bp DNA linear PAT 16-MAY-2001  
 LOCUS DEFINITION Sequence 1820 from patent US 6194150.  
 VERSION ARI33395  
 KEYWORDS ARI33395.1 GI:14122300  
 SOURCE UNKNOWN.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
 TITLE Nucleic acid based inhibition of CD40  
 JOURNAL Patent: US 6194150-A 1820 27-FEB-2001;  
 FEATURES Location/Qualifiers  
 source 1..15  
 BASE COUNT 4 a 3 c 2 g 6 t  
 ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9  
 |||||  
 DB 12 TTCTGAGAA 4

RESULT 3  
 AX277553 18 bp DNA linear PAT 01-NOV-2001  
 LOCUS DEFINITION Sequence 32 from Patent WO0177327.  
 VERSION AX277553  
 KEYWORDS AX277553.1 GI:16604752  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct  
 REFERENCE 1 (sites)  
 AUTHORS Carulli,J.P., Little,R.D., Becker,R.R. and Johnson,M.L.  
 TITLE The high bone mass gene of 11q13.3  
 JOURNAL Patent: WO 0177327-A 32 18-OCT-2001;  
 FEATURES Genome Therapeutics Corporation (US)  
 source 1..18  
 BASE COUNT 5 a 5 c 4 g 4 t  
 ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9  
 |||||  
 DB 6 TTCTGAGAA 14

RESULT 4  
 ARO43730/c 19 bp DNA linear PAT 29-SEP-1999  
 LOCUS DEFINITION Sequence 100 from patent US 5814517.  
 VERSION ARO43730.1 GI:5964738  
 KEYWORDS UNKNOWN.  
 SOURCE UNKNOWN.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Seidel,H.,Martin. and Lamb,I.,Peter.  
 TITLE DNA spacer regulatory elements responsive to cytokines and methods  
 JOURNAL Patent: US 5814517-A 100 29-SEP-1998;  
 FEATURES Location/Qualifiers  
 source 1..19  
 BASE COUNT 4 a 5 c 4 g 6 t  
 ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9  
 |||||  
 DB 16 TTCTGAGAA 8

RESULT 5  
 ARO43731 19 bp DNA linear PAT 29-SEP-1999  
 LOCUS DEFINITION Sequence 101 from patent US 5814517.  
 VERSION ARO43731  
 KEYWORDS ARO43731.1 GI:5964739  
 SOURCE UNKNOWN.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Seidel,H.,Martin. and Lamb,I.,Peter.  
 TITLE DNA spacer regulatory elements responsive to cytokines and methods  
 JOURNAL Patent: US 5814517-A 101 29-SEP-1998;  
 FEATURES Location/Qualifiers  
 source 1..19  
 BASE COUNT 6 a 4 c 5 g 4 t  
 ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9  
 |||||  
 DB 8 TTCTGAGAA 16

RESULT 6  
 AX130312 19 bp DNA linear PAT 15-MAY-2001  
 LOCUS DEFINITION Sequence 1530 from Patent WO0130362.  
 VERSION AX130312  
 KEYWORDS AX130312.1 GI:14136617  
 SOURCE human.  
 ORGANISM Homo sapiens  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 AUTHORS Robbins,J.M. and Tritz,R.  
 TITLE Ridozyme therapy for the treatment of proliferative skin and eye

diseases  
 Patent: WO 0130362-A 1530 03-MAY-2001;  
 IMMUSOL, INC. (US)  
 Location/Qualifiers  
 FEATURES  
 source 1..19  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /note="Cyclin A2 ribozyme binding site"  
 BASE COUNT 8 a 2 c 5 g 4 t  
 ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
 |||||||  
 Db 9 TTCTGAGAA 17

RESULT 7  
 LOCUS 181958 19 bp DNA linear PAT 10-JUN-1998  
 DEFINITION Sequence 56 from patent US 5712094.  
 ACCESSION 181958  
 VERSION 181958.1 GI:3210255  
 KEYWORDS  
 SOURCE .  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Seidel,H.Martin., Lamb,I.Peter. and Chan,S.-S.Tian.  
 TITLE Methods for detecting modulators of cytokine action  
 JOURNAL Patent: US 5712094-A 56 27-JAN-1998;  
 FEATURES  
 source 1..19  
 /organism="unknown"  
 BASE COUNT 4 a 5 c 4 g 6 t  
 ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
 |||||||  
 Db 16 TTCTGAGAA 8

RESULT 8  
 LOCUS 181959 19 bp DNA linear PAT 10-JUN-1998  
 DEFINITION Sequence 57 from patent US 5712094.  
 ACCESSION 181959  
 VERSION 181959.1 GI:3210256  
 KEYWORDS  
 SOURCE .  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Seidel,H.Martin., Lamb,I.Peter. and Chan,S.-S.Tian.  
 TITLE Methods for detecting modulators of cytokine action  
 JOURNAL Patent: US 5712094-A 57 27-JAN-1998;  
 FEATURES  
 source 1..19  
 /organism="unknown"  
 BASE COUNT 6 a 4 c 5 g 4 t  
 ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
 |||||||  
 Db 8 TTCTGAGAA 16

RESULT 9  
 LOCUS A67540 20 bp DNA linear PAT 05-MAY-1999  
 DEFINITION Sequence 21 from Patent W09743647.  
 ACCESSION A67540  
 VERSION A67540.1 GI:4756420  
 KEYWORDS  
 SOURCE .  
 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS La,T.N. and De,L.L.  
 TITLE DP AND E2F PROTEIN NUCLEAR LOCALISATION SIGNALS AND THEIR USE  
 JOURNAL Patent: WO 9743647-A 21 20-NOV-1997;  
 MEDICAL RES COUNCIL (GB)  
 FEATURES  
 source 1..20  
 /organism="unidentified"  
 /db\_xref="taxon:32644"  
 BASE COUNT 7 a 3 c 4 g 6 t  
 ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
 |||||||  
 Db 1 TTCTGAGAA 9

RESULT 10  
 LOCUS AR029053 20 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 21 from patent US 5859199.  
 ACCESSION AR029053  
 VERSION AR029053.1 GI:5941026  
 KEYWORDS  
 SOURCE .  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS La,Thanhue,N.B. and de la Luna,S.  
 TITLE Transcription factor DP-3 and isoforms thereof  
 JOURNAL Patent: US 5859199-A 21 12-JAN-1999;  
 FEATURES  
 source 1..20  
 /organism="unknown"  
 BASE COUNT 7 a 3 c 4 g 6 t  
 ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
 |||||||  
 Db 1 TTCTGAGAA 9

RESULT 11  
 LOCUS AR120696 20 bp DNA linear PAT 16-MAY-2001

```

DEFINITION Sequence 21 from patent US 6159691.
ACCESSION ARI20696
VERSION ARI20696.1 GI:14104272
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS La Thangue,N.D. and De La Luna,S.
TITLE Assay for a putative regulator of cell cycle progression
JOURNAL Patent: US 6159691-A 21 12-DEC-2000;
FEATURES
source
1..20
location/Qualifiers
BASE COUNT 7 a 3 c 4 g 6 t
ORIGIN
Query Match 100.0%; Score 9; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ttctgagaa 9
|||||
DB 1 TTCTGAGAA 9

RESULT 12
E03365 20 bp DNA linear PAT 29-SEP-1997
LOCUS E03365
DEFINITION Oligonucleotide for detection of human papilloma virus gene.
ACCESSION E03365
VERSION E03365.1 GI:2171582
KEYWORDS JP 1992058888-A/2.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE
1 (bases 1 to 20)
AUTHORS Yoshie,O. and Mak1,H.
TITLE OLIGONUCLEOTIDE FOR DETECTING HUMAN PAPILLOMA VIRUS GENE AND
JOURNAL DETECTION METHOD USING THE SAME
PATENT: JP 1992058888-A 2 25-FEB-1992;
SHIONOGI & CO LTD
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1992058888-A/2
PD 25-FEB-1992
PE 28-JUN-1990 JP 1990171986
PI YOSHIE OSAMU, MAKI HIDEO
PC C12N15/11,C07H21/00,C12Q1/68,G01N33/569,G01N33/574; CC
strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FEATURES
source
1..20
location/Qualifiers
BASE COUNT 5 a 2 c 8 g 5 t
ORIGIN
Query Match 100.0%; Score 9; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ttctgagaa 9
|||||
DB 4 TTCTGAGAA 12

RESULT 13
AR040919

```

```

LOCUS AR040919 22 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 18 from patent US 5811238.
ACCESSION AR040919
VERSION AR040919.1 GI:5961415
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 22)
AUTHORS Stemmer,W.P.C. and Cramer1,A.
TITLE Methods for generating polynucleotides having desired
JOURNAL characteristics by iterative selection and recombination
PATENT: US 5811238-A 18 22-SEP-1998;
FEATURES
source
1..22
location/Qualifiers
BASE COUNT 8 a 4 c 3 g 7 t
ORIGIN
Query Match 100.0%; Score 9; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ttctgagaa 9
|||||
DB 13 TTCTGAGAA 21

RESULT 14
AR051826 22 bp DNA linear PAT 29-SEP-1999
LOCUS AR051826
DEFINITION Sequence 18 from patent US 5830721.
ACCESSION AR051826
VERSION AR051826.1 GI:5975190
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 22)
AUTHORS Stemmer,W.P.C. and Cramer1,A.
TITLE DNA mutagenesis by random fragmentation and reassembly
JOURNAL Patent: US 5830721-A 18 03-NOV-1998;
FEATURES
source
1..22
location/Qualifiers
BASE COUNT 8 a 4 c 3 g 7 t
ORIGIN
Query Match 100.0%; Score 9; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ttctgagaa 9
|||||
DB 13 TTCTGAGAA 21

RESULT 15
AR115962 22 bp DNA linear PAT 16-MAY-2001
LOCUS AR115962
DEFINITION Sequence 18 from patent US 6132970.
ACCESSION AR115962
VERSION AR115962.1 GI:14096284
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 22)
AUTHORS Stemmer,W.P.C.
TITLE Methods of shuffling polynucleotides
JOURNAL Patent: US 6132970-A 18 17-OCT-2000;

```

FEATURES                      Location/Qualifiers  
          source                      1. .22  
BASE COUNT                      8 a                      4 c                      3 g                      7 t  
ORIGIN

Query Match                      100.0%; Score 9; DB 6; Length 22;  
Best Local Similarity              100.0%; Pred. No. 1.1e+05;  
Matches                      9; Conservative              0; Mismatches              0; Indels              0; Gaps              0;

QY                      1 ttctgagaa 9  
                          |||||  
DB                      13 TTCCTGAGAA 21

Search completed: August 20, 2002, 23:23:03  
Job time: 6574 sec

**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 22:26:44 ; Search time 206.01 Seconds  
(without alignments)  
75.007 Million cell updates/sec

Title: NA\_SEQ  
Perfect score: 9  
Sequence: 1 tctcgagaa 9

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 1662488

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N.Geneseq.032802:\*

1: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1994.DAT:\*  
16: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT:\*  
17: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT:\*  
18: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	9	16	AAT14149	Cytokine responsive
2	100.0	9	17	AAT14583	Cytokine activated
3	100.0	9	19	AAV56876	Regulatory element
4	100.0	9	15	AAK66325	Mouse B7-2 hammetrh
5	100.0	15	17	AAK66326	Mouse B7-2 hammetrh
6	100.0	17	21	AAF02601	Hammerhead ribozym
7	100.0	17	21	AAF02602	Hammerhead ribozym
8	100.0	17	21	AAF02603	Hammerhead ribozym
9	100.0	17	21	AA36041	Human genomic SNP

C	10	9	100.0	18	19	AAV24227	primer alpha(1)a f
C	11	9	100.0	18	19	AAV24228	primer alpha(1)b f
C	12	9	100.0	18	22	ABA82604	HBM1 polymorphism
C	13	9	100.0	18	22	ABA82646	Human zmax1 PCR pr
C	14	9	100.0	19	17	AAT41612	Oligonucleotide co
C	15	9	100.0	19	19	AAV56841	Regulatory element
C	16	9	100.0	19	19	AAV56942	Regulatory element
C	17	9	100.0	19	21	AAAB3944	Cyclin A2 ribozyme
C	18	9	100.0	19	22	AAH59106	Cyclin A2 ribozyme
C	19	9	100.0	20	13	AAO23061	HepV-16 primer (2).
C	20	9	100.0	20	16	AAO91527	ETS-2 Mspr RFLP pr
C	21	9	100.0	20	19	AAH88330	Human E2-A for mu
C	22	9	100.0	20	20	AAV80051	Human PMW2 Intron
C	23	9	100.0	20	21	AAZ45501	PCR primer used to
C	24	9	100.0	20	21	AAZ36354	PCR primer 649419-
C	25	9	100.0	21	22	AAH62317	Histamine receptor
C	26	9	100.0	21	22	AAAF7401	Primer #35. Homo
C	27	9	100.0	22	18	AAAT73036	Mutagenic PCR prim
C	28	9	100.0	22	19	AAV54907	Primer used for int
C	29	9	100.0	22	20	AAV33878	PCR primer for B6/
C	30	9	100.0	22	22	AAAD18956	PCR primer #14 to
C	31	9	100.0	23	18	AAV01403	Primer AR for dete
C	32	9	100.0	23	18	AAAT72679	PIR-related kinase
C	33	9	100.0	23	18	AAAF61980	Human ATR gene pri
C	34	9	100.0	23	19	AAAX10121	Human biallelic po
C	35	9	100.0	23	21	AAAB8084	Citrus viroid II d
C	36	9	100.0	23	21	AAAT2057	Japanese citrus vi
C	37	9	100.0	23	21	AAZ37849	PCR primer ODH26 f
C	38	9	100.0	23	22	AAH46729	Type 11 phosphodie
C	39	9	100.0	24	18	AAH59391	Human papilloma vi
C	40	9	100.0	24	20	AAAX57032	S. pneumoniae phes
C	41	9	100.0	24	20	AAAX36324	PCR primer used to
C	42	9	100.0	24	21	AAAX5486	Myrtaceae microsat
C	43	9	100.0	24	21	AAZ37061	CDNA encoding a MH
C	44	9	100.0	24	21	AAZ37068	CDNA encoding a pe
C	45	9	100.0	24	21	AAZ37069	CDNA encoding a pe

ALIGNMENTS

RESULT 1	
AAT14149/c	
ID AAT14149 standard; DNA; 9 BP.	
XX	
XX AAT14149;	
XX	
DT 29-MAY-1996 (first entry)	
XX	
DE Cytokine responsive DNA spacer regulatory element.	
XX	
KW Regulatory element; transcriptional regulatory protein;	
KW signalling molecule; DNA spacer; agonist; antagonist; anaemia;	
KW gene transcription; inflammation; cytopenia; cancer; ss.	
XX	
OS Synthetic.	
PN WO9528482-A2.	
XX	
PD 26-OCT-1995.	
XX	
PF 10-APR-1995; 95WO-US04477.	
XX	
PR 27-MAR-1995; 95US-0410780.	
PR 14-APR-1994; 94US-0228935.	
XX	
PA (LIGA-) LIGAND PHARM INC.	
XX	
PI Lamb IP, Seidel HM;	
XX	
DR WPI; 1995-373797/48.	
XX	
PT DNA spacer regulatory elements responsive to cytokine(s) - for	

PT detecting the presence of transcriptional regulatory protein in a  
sample  
XX  
XX  
PS Claim 7; Page 125; 135pp; English.  
XX  
CC The present oligonucleotide comprises a regulatory element  
CC TTT(Nx)AA, where x is 4-7, and the regulatory element binds an  
CC activated transcriptional regulatory protein in response to a  
CC signalling mol., i.e. a cytokine. This cytokine responsive DNA  
CC spacer regulatory element can be used to detect the presence of  
CC a transcriptional regulatory protein in a sample, and in assays  
CC for (anti)agonists of gene transcription. The identified cpds.  
CC may be used to treat cytokine-induced disease states, or to  
CC ameliorate disease states caused by cytokine deficiency, e.g.  
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.  
XX  
SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 16; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+08;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
|||||  
DB 9 TTCTGAGAA 1

RESULT 2  
AAV41583/C  
ID AAV41583 standard; DNA: 9 BP.  
XX  
AC AAV41583;  
XX  
DT 04-JUN-1997 (first entry)  
XX  
DE Cytokine activated STAT protein dependent DNA regulatory element.  
XX  
KM Regulatory element; protein: cytokine; responsive; host cell;  
KM transfection; agonist; antagonist; mediated; transcription;  
KM modulation; STAT; STAT5; STAT6; signalling pathway; ss.  
XX  
OS Synthetic.  
XX  
PN WO9630515-A1.  
XX  
PD 03-OCT-1996.  
XX  
PE 25-MAR-1996; 96WO-US04012.  
XX  
PR 27-MAR-1995; 95US-0411020.  
XX  
PA (LIGA-) LIGAND PHARM INC.  
XX  
PI Lamb IP, Seidel HM, Tian Chan S;  
XX  
DR WPI: 1996-455362/45.  
XX  
PT DNA construct for screening modulators of cytokine-mediated  
PT transcription - contg. regulatory element and a cytokine-sensitive  
PT promoter operably linked to a heterologous gene  
XX  
PS Claim 5; Page 61; 72pp; English.  
XX  
CC A novel DNA construct comprises an oligonucleotide (ON) comprising  
CC a regulatory element having the present sequence, operably linked  
CC to a promoter, which is operably linked to a heterologous gene  
CC (preferably a marker gene). The gene is under the transcriptional  
CC control of the promoter and the ON sequence when the ON is bound by  
CC a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,  
CC erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,  
CC IL-13 or IL-15. Cytokine responsive host cells transfected with the  
CC DNA construct can be used to measure the ability of a compound to

CC act as an agonist or antagonist of cytokine mediated gene  
CC transcription. In particular, they can be used to screen for  
CC cytokine modulators involved in the STATs and/or STAT6 protein  
CC signalling pathway.  
XX  
SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 17; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+08;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
|||||  
DB 9 TTCTGAGAA 1

RESULT 3  
AAV56876/C  
ID AAV56876 standard; DNA: 9 BP.  
XX  
AC AAV56876;  
XX  
DT 02-DEC-1998 (first entry)  
XX  
DE Regulatory element containing oligonucleotide #35.  
XX  
KM Cytokine-responsive regulatory; primer; promoter; detection; isolation;  
KM transcriptional control; STAT protein; screening; agonist; ss.  
XX  
OS Synthetic.  
XX  
PN US5814517-A.  
XX  
PD 29-SEP-1998.  
XX  
PE 27-MAR-1995; 95US-0410779.  
XX  
PR 27-MAR-1995; 95US-0410779.  
PR 14-APR-1994; 94US-0228935.  
XX  
PA (LIGA-) LIGAND PHARM INC.  
XX  
PI Lamb IP, Seidel HM;  
XX  
DR WPI: 1998-541763/46.  
XX  
PT DNA constructs containing cytokine-responsive regulatory elements -  
PT useful in assays for transcription-regulating proteins or gene  
PT transcription agonists or antagonists  
XX  
PS Disclosure; Column 11; 58pp; English.  
XX  
CC AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the  
CC production of constructs comprising a cytokine-responsive regulatory  
CC element linked to a promoter which is linked to a heterologous coding  
CC sequence so that the coding sequence is under the transcriptional  
CC control of the regulatory element and the promoter, where the regulatory  
CC element has a nucleotide sequence selected from TTGNGAA, TTANYTAA, and  
CC TTGNYTAA where N is A, T, C or G, and y = 3 or 4. The constructs can be  
CC used to detect or isolate transcription-regulating proteins, e.g. STAT  
CC proteins, in a sample by contacting the sample with the construct so that  
CC the protein binds to the regulatory element, and detecting or separating  
CC the resulting complex. The cells can be used in screening assays for  
CC agonists of gene transcription, in which the level of expression of the  
CC coding sequence is measured in the presence and absence of a test  
CC compound or in the presence of the corresponding cytokine.  
XX  
SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+08;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
 |||  
 XX 9 TTCTGAGAA 1

Db 9 TTCTGAGAA 1

RESULT 4  
 AAX66325/C  
 ID AAX66325 standard; RNA; 15 BP.

XX AAX66325;  
 AC  
 XX 20-JUL-1999 (first entry)  
 DT  
 XX  
 DE Mouse B7-2 hammerhead ribozyme target SEQ ID NO:2957.

XX  
 KM Arthritic condition; graft tolerance; immune response; target; cleavage;  
 KM hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
 KM stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
 KM rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
 KM diagnosis; ss.

XX  
 OS Mus sp.  
 XX  
 PN WO9618736-A2.  
 XX  
 PD 20-JUN-1996.  
 XX  
 PF 22-NOV-1995; 95WO-US15516.

XX  
 PR 05-OCT-1995; 95US-0541365.  
 PR 13-DEC-1994; 94US-0354920.  
 PR 23-DEC-1994; 94US-0363253.  
 PR 23-DEC-1994; 94US-0363254.  
 PR 17-FEB-1995; 95US-0390850.  
 PR 20-APR-1995; 95US-0426124.  
 PR 02-MAY-1995; 95US-0432874.  
 PR 04-MAY-1995; 95US-0434509.  
 PR 07-JUL-1995; 95US-0000951.  
 PR 07-JUL-1995; 95US-0000974.  
 PR 07-AUG-1995; 95US-0512861.

XX  
 PA (RIBO-) RIBOZYME PHARM INC.

PI Draper K, Gustofson J, McSwigen J, Pavco P, Stinchcomb DT;  
 PI Beigelman L, Karpelsky A, Modak A, Usman N, Burgin A;  
 PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;  
 XX  
 DR WPI; 1996-300653/30.

XX  
 PT Enzymatic nucleic acid molecules having a hammer-head motif - used  
 PT for the treatment of arthritis; induction of graft tolerance or  
 PT treatment of auto-immune diseases

XX  
 PS Claim 10; Page 198; 307pp; English.

XX  
 CC The present invention describes a novel enzymatic nucleic acid (ENA)  
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose  
 CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)  
 CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.  
 CC The ENA's can inhibit collagenase and stromelysin production in the  
 CC synovial membrane of joints for the treatment or prevention of arthritis,  
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
 CC be used to treat antigen presenting cells of a donor to induce tolerance  
 CC in a recipient to an alloantigen of a donor. They can also be used for  
 CC enhancing graft tolerance or for treating autoimmune disease, and for  
 CC treating allergies and other inflammatory conditions. The ENA's can also  
 CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
 CC stromelysin without introducing the non-specific effects upon gene  
 CC expression which accompany treatment with retinoids and dexamethasone.  
 CC The concentration of ribozyme required to affect a therapeutic treatment  
 CC is lower than that required of antisense molecules, and is highly

CC specific. The present sequence is used in the exemplification of the  
 CC present invention.

XX  
 SQ Sequence 15 BP; 5 A; 3 C; 3 G; 4 U; 0 other;

Query Match 100.0%; Score 9; DB 17; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
 |||  
 XX 15 TTCTGAGAA 7

Db 15 TTCTGAGAA 7

RESULT 5  
 AAX66326/C  
 ID AAX66326 standard; RNA; 15 BP.

XX AAX66326;  
 AC  
 XX 20-JUL-1999 (first entry)  
 DT  
 XX  
 DE Mouse B7-2 hammerhead ribozyme target SEQ ID NO:2958.

XX  
 KM Arthritic condition; graft tolerance; immune response; target; cleavage;  
 KM hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
 KM stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
 KM rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
 KM diagnosis; ss.

XX  
 OS Mus sp.  
 XX  
 PN WO9618736-A2.  
 XX  
 PD 20-JUN-1996.  
 XX  
 PF 22-NOV-1995; 95WO-US15516.

XX  
 PR 05-OCT-1995; 95US-0541365.  
 PR 13-DEC-1994; 94US-0354920.  
 PR 23-DEC-1994; 94US-0363253.  
 PR 23-DEC-1994; 94US-0363254.  
 PR 17-FEB-1995; 95US-0390850.  
 PR 20-APR-1995; 95US-0426124.  
 PR 02-MAY-1995; 95US-0432874.  
 PR 04-MAY-1995; 95US-0434509.  
 PR 07-JUL-1995; 95US-0000951.  
 PR 07-JUL-1995; 95US-0000974.  
 PR 07-AUG-1995; 95US-0512861.

XX  
 PA (RIBO-) RIBOZYME PHARM INC.

PI Draper K, Gustofson J, McSwigen J, Pavco P, Stinchcomb DT;  
 PI Beigelman L, Karpelsky A, Modak A, Usman N, Burgin A;  
 PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;  
 XX  
 DR WPI; 1996-300653/30.

XX  
 PT Enzymatic nucleic acid molecules having a hammer-head motif - used  
 PT for the treatment of arthritis; induction of graft tolerance or  
 PT treatment of auto-immune diseases

XX  
 PS Claim 10; Page 198; 307pp; English.

XX  
 CC The present invention describes a novel enzymatic nucleic acid (ENA)  
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose  
 CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)  
 CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.  
 CC The ENA's can inhibit collagenase and stromelysin production in the  
 CC synovial membrane of joints for the treatment or prevention of arthritis,  
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
 CC be used to treat antigen presenting cells of a donor to induce tolerance

CC in a recipient to an allergen of a donor. They can also be used for  
CC enhancing graft tolerance or for treating autoimmune disease, and for  
CC treating allergies and other inflammatory conditions. The ENA's can also  
CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
CC streptomycin without introducing the non-specific effects upon gene  
CC expression which accompany treatment with tetracyclins and dexamethasone.  
CC The concentration of ribozymes required to affect a therapeutic treatment  
CC is lower than that required of antisense molecules, and is highly  
CC specific. The present sequence is used in the exemplification of the  
CC present invention.

CC  
CC  
CC Sequence 15 BP; 4 A; 3 C; 2 G; 6 U; 0 other;  
CC  
CC

Query Match	100.0%	Score 9	DB 17	Length 15
Best Local Similarity	100.0%	Pred. No. 9	5c+03	
Matches	9	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
Oy	1	tctctagaaa	9	
Db	12	TTCTCTGAGAA	4	

XX	AA02601/c
XX	AA02601 standard; DNA; 17 BP.
XX	AA02601;
XX	16-FEB-2001 (first entry)
XX	Hammerhead ribozyme substrate #896.
XX	Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX	interferon alpha; ss.
XX	Homo sapiens.
XX	MO200061729-A2.
XX	19-OCT-2000.
XX	11-APR-2000; 2000MO-US09721.
XX	12-APR-1999; 99US-0129390.
XX	(RIBO-) RIBOZYME PHARM INC.
XX	Blatt L, Zwick M, Pavco P, McSwigen J;
XX	WPI; 2000-647423/62.
XX	Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX	useful for producing e.g. granulocyte colony stimulating factor
XX	protein, interferon alpha and erythropoietin -
XX	Claim 37; Page 76; 164pp; English.
XX	The present invention relates to enzymatic and antisense nucleic acid
XX	molecules that act as inhibitors of the expression of repressor genes
XX	encoding the TR2 Orphan receptor, EAR3/COP-Tr-1, the GATA
XX	transcription factor gene, IRF-2 and/or the CATT Displacement
XX	inhibition (CDP). Inhibition of the repressors removes prevents
XX	inhibition (and consequently increases expression of) genes involved in
XX	the production of erythropoietin, granulocyte colony stimulating factor
XX	protein and interferon alpha.
XX	Sequence 17 BP; 5 A; 4 C; 4 G; 4 T; 0 other;

Query Match	100.0%	Score 9;	DB 21;	Length 17;
Best Local Similarly	100.0%;	Pred. No. 9;	Se+03;	
Matches	9;	Conservative	0;	Indels 0;
				Gaps 0;

Qy	1	ttcttgagaa	9
Db	16	ttcttcagaa	8
RESULT 7			
AAAF02602/c			
ID	AAAF02602 standard; DNA; 17 BP.		

XX	RESULT	7
XX	AAf02602/c	
XX	ID	AAf02602 standard; DNA; 17 BP.
XX	AC	
XX	AAf02602;	
XX	DT	
XX	DE	16-FEB-2001 (first entry)
XX	DE	Hammerhead ribozyme substrate #897.
XX	KM	Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX	KM	Interferon alpha; ss.
XX	OS	
XX	Homo	sapiens.
XX	PN	WO200061729-A2.
XX	PD	
XX	PD	19-OCT-2000.
XX	PE	
XX	PR	11-APR-2000; 2000WO-US09721.
XX	PA	12-APR-1999; 99US-0129390.
XX	(RIBO-)	RIBOZYME PHARM INC.
XX	Blatt L,	Zwick M, Pavco P, McSwiggen J;
XX	WPI;	2000-647423/62.
XX	DR	
PT	Enzymatic	and antisense nucleic acid inhibition of repressor genes,
PT	useful	for producing e.g. granulocyte colony stimulating factor
XX	protein,	interferon alpha and erythropoietin -
PS	Claim 37;	Page 76; 164pp; English.
XX	XX	
CC	The present invention relates to enzymatic and antisense nucleic acid	
CC	molecules that act as inhibitors of the expression of repressor genes	
CC	encoding the TR2 Orphan receptor, EAR3/CODP-TR-1, the GATA	
CC	transcription factor gene, IRF-2 and/or the CAAT Displacement	
CC	Protein (CDP). Inhibition of the repressors removes prevents	
CC	inhibition (and consequently increases expression of) genes involved in	
CC	the production of erythropoietin, granulocyte colony stimulating factor	
CC	protein and interferon alpha.	
SQ	Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;	

Query Match	100.0%	Score 9:	DB 21:	Length 17:
Best Local Similarity	100.0%	Pred. No.	9.5e+03:	
Matches 9:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:

QY	1	ttctgagaa	9
Db	15	TtCTGAGAA	7
RESULT	8		
AAE02603/C			
ID	AAE02603	standard; DNA; 17 BP	

RESULT 8  
AAf02603/c  
ID AAf02603 standard; DNA; 17 BP.  
XX  
XX  
AC AAf02603;  
XX  
XX  
DT 16-FEB-2001 (first entry)  
XX  
XX  
DE Hammerhead ribozyme substrate #898.  
XX  
XX  
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;

```

KM interferon alpha; ss.
XX
XX OS Homo sapiens.
XX PN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwigen J;
XX WPI; 2000-647423/62.
XX DR
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor
XX protein, interferon alpha and erythropoietin -
XX
XX PS Claim 37; Page 76; 164pp; English.
XX
XX CC The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRF-2 and/or the CCAAT displacement
XX protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.
XX
XX SQ Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 other;

Query Match          100.0%; Score 9; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
   |||||||
Db 13 TTCTGAGAA 5

RESULT 9
AAA36041
ID AAA36041 standard; DNA; 17 BP.
AC AAA36041;
XX
XX DT 26-JUL-2000 (first entry)
XX DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:38.
XX
XX KW Human: single nucleotide polymorphism; SNP; genotyping; DNA analysis;
XX allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
XX genomic classification; identification; DNA fingerprinting;
XX tumour characterisation; hybridisation; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200018960-A2.
XX PD 06-APR-2000.
XX PF 24-SEP-1999; 99WO-US22283.
XX PR 25-SEP-1998; 98US-0101757.
XX PA (MAST) MASSACHUSETTS INST TECHNOLOGY.
XX PI Landers JE, Jordan B, Housman DE, Charest A;

```

```

XX WPI; 2000-293181/25.
XX DR
XX PT Detection of single nucleotide polymorphisms in genomes by preparation
XX and analysis of reduced complexity genomes, useful for genotyping,
XX fingerprinting and determining allele frequency of SNPs -
XX
XX PS Disclosure; Page 56; 111pp; English.
XX
XX CC A method has been developed for detecting the presence or absence of a
XX single nucleotide polymorphism (SNP) allele in a genomic sample. The
XX method comprises preparing a reduced complexity genome (RCG) from the
XX genomic sample and analysing the RCG for the presence or absence of a
XX SNP allele. The method can be used to characterise a tumour, to generate
XX a genomic pattern for an individual genome or to generate a genomic
XX classification code for a genome. The method can be used to assess
XX whether a subject is at risk for developing a disease or to identify a
XX set of SNP alleles associated with a disease. The method can also be
XX used to perform linkage analysis. AAA35944 to AAA35947 represent
XX sequences used in the exemplification of the present invention. AAA35948
XX to AAA36632 represent nucleotide sequences containing SNPs.
XX
XX SQ Sequence 17 BP; 4 A; 1 C; 4 G; 8 T; 0 other;

Query Match          100.0%; Score 9; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
   |||||||
Db 1 ttctgagaa 9

RESULT 10
AAV24227/C
ID AAV24227 standard; DNA; 18 BP.
XX
XX AC AAV24227;
XX
XX DT 12-AUG-1998 (first entry)
XX DE Primer alpha(1)a for human alphoid DNA sequence.
XX
XX KW CENP-B box; mammalian artificial chromosome; MAC; chromosome 21;
XX mammalian telomere; centromere; yeast artificial chromosomes; YAC;
XX somatic gene therapy; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO9808964-A1.
XX PD 05-MAR-1998.
XX PF 26-AUG-1996; 96WO-JP02381.
XX PR 26-AUG-1996; 96WO-JP02381.
XX PA (KENO/) IKENO M.
XX PA (MASU/) MASUMOTO H.
XX PA (OKAZ/) OKAZAKI T.
XX
XX PI Cooke HJ, Grimes BR, Ikeno M, Masumoto H, Okazaki T;
XX WPI; 1998-216941/19.
XX DR
XX PT Mammalian artificial chromosomes - prepared using DNA construct
XX comprising mammalian telomere and centromere containing copies of
XX CENP-B box sequences
XX
XX PS Disclosure; Page 34; 95pp; English.

```

RESULT	11
AAV24228	
ID	AAV24228 standard; DNA; 18 BP.
XX	
AC	AAV24228;
XX	
DT	12-AUG-1998 (first entry)
XX	
DE	Primer alpha(1)b for human alphoid DNA sequence.
XX	
KM	CENP-B box; mammalian artificial chromosome; MAC; chromosome 21;
KW	mammalian telomere; centromere; yeast artificial chromosomes; YAC;
KW	somatic gene therapy; PCR primer; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	W09808964-A1.
XX	
PD	05-MAR-1998.
XX	
PF	26-AUG-1996; 96MO-JP02381.
XX	
PR	26-AUG-1996; 96MO-JP02381.
XX	
PA	(KENO/) IKENO M.
PA	(MASU/) MASUMOTO H.
PA	(OKAZ/) OKAZAKI T.
XX	
XX	Cooke HJ, Grimes BR, Ikono M, Masumoto H, Okazaki T;
XX	
DR	WPI; 1998-216941/19.
XX	
PT	Mammalian artificial chromosomes - prepared using DNA construct
PT	comprising mammalian telomere and centromere containing copies of
PT	CENP-B box sequences
XX	
PS	Disclosure; Page 34; 95pp; English.
XX	
CC	This sequence is a primer for a human alphoid DNA sequence that can be

RESULT 12	
ABAB82604	
ID	ABAB82604 standard; DNA; 18 BP.
XX	
AC	ABA82604;
XX	
DT	25-JAN-2002 (first entry)
XX	
DE	HBW1 polymorphism containing amplicon PCR primer 1863P.
XX	
KW	Human, high bone mass; HBM gene; chromosome 11; 11q13.3;
KW	sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW	antlense therapy; vaccine; bone disorder; Paget's disease; adapter;
XX	sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX	
OS	Homo sapiens.
OS	synthetic.
XX	
PN	WO200177327-A1.
XX	
PD	18-OCT-2001.
XX	
PP	21-JUN-2000; 2000WO-US16951.
XX	
PP	05-APR-2000; 2000US-0543771.
PR	05-APR-2000; 2000US-0544398.
XX	
PA	(GENO-) GENOME THERAPEUTICS CORP.
XX	
PI	Carulli JP, Little RD, Recker RR, Johnson ML,
DR	WPL; 2001-657171/75.
XX	
PT	New high bone mass (HBM) and Zmax1 genes and proteins useful for
XX	modulating bone mass for the treatment of e.g. osteoporosis -
PS	Disclosure; Page 63; 443pp; English.
XX	
CC	The present invention describes the human Zmax1 gene and the high bone
CC	mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and
CC	HBM genes have osteopathic activities. The genes can be used in gene

CC therapy, antitense therapy and in the production of vaccines. They  
 CC can be used in the diagnosis and treatment of bone disorders including  
 CC osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous  
 CC dysplasia. ABA82038 to ABA82700 and AAG68168 to AAG68193 represent  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 9; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
 |||||  
 Db 6 ttctgagaa 14

## RESULT 13

ABA82646  
 ID ABA82646 standard; DNA; 18 BP.

AC ABA82646;

DT 25-JAN-2002 (first entry)

DE Human Zmax1 PCR primer SEQ ID NO:32.

XX Human: high bone mass; HBM gene; zmax1 gene; chromosome 11; 11q13.3;

KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;

KW antitense therapy; vaccine; bone disorder; Paget's disease; adapter;

KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.

XX Homo sapiens.

OS Synthetic.

XX MO200177327-A1.

PD 18-OCT-2001.

XX 21-JUN-2000; 2000MO-US16951.

XX 05-APR-2000; 2000US-0543771.

PR 05-APR-2000; 2000US-0544398.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Carulli JP, Little RD, Recker RR, Johnson ML;

DR WPI; 2001-657171/75.

XX New high bone mass (HBM) and zmax1 genes and proteins useful for

PT modulating bone mass for the treatment of e.g. osteoporosis -

PS Disclosure; Page 103; 443pp; English.

XX The present invention describes the human zmax1 gene and the high bone

CC mass (HBM) gene, which are found on chromosome 11q13.3. The zmax1 and

CC HBM genes have osteopathic activities. The genes can be used in gene

CC therapy, antitense therapy and in the production of vaccines. They

CC can be used in the diagnosis and treatment of bone disorders including

CC osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous

CC dysplasia. ABA82038 to ABA82700 and AAG68168 to AAG68193 represent

CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 other;

Db 6 ttctgagaa 14  
 |||||

## RESULT 14

ATA41612/C

ID ATA41612 standard; DNA; 19 BP.

AC ATA41612;

DT 04-JUN-1997 (first entry)

DE Oligonucleotide containing core DNA regulatory element.

XX Regulatory element; SPAT; protein; cytokine; responsive;

KW host cell; transfection; agonist; antagonist; mediated; STAT5;

KW transcription; modulation; signalling pathway; STAT6;

KW oligonucleotide; electrophoretic mobility shift assay; EMSA; ds.

XX Synthetic.

XX Key

XX Location/Qualifiers

FT misc\_feature 5..19

FT /tag= a

FT /note= "core DNA regulatory element"

XX MO9630515-A1.

XX 03-OCT-1996.

XX 25-MAR-1996; 96MO-US04012.

XX 27-MAR-1995; 95US-0411020.

XX (LIGA-) LIGAND PHARM INC.

XX Lamb IP, Seidel HM, Tian Chan S;

XX WPI; 1996-455362/45.

XX DNA construct for screening modulators of cytokine-mediated

PT transcription - contg. regulatory element and a cytokine-sensitive

PT promoter operably linked to a heterologous gene

XX Example 1; Page 26; 72pp; English.

XX A novel DNA construct comprises the present oligonucleotide (ON),

CC which contains a core a regulatory element, operably linked to a

CC promoter, which is operably linked to a heterologous gene

CC (preferably a marker gene). The gene is under the transcriptional

CC control of the promoter and the ON sequence when the ON is bound by

CC a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,

CC erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,

CC IL-13 or IL-15. Cytokine responsive host cells transfected with the

CC DNA construct can be used to measure the ability of a compound to

CC act as an agonist or antagonist of cytokine mediated gene

CC transcription. In particular, they can be used to screen for

CC cytokine modulators involved in the STAT5 and/or STAT6 protein

CC signalling pathway.

CC Following an electrophoretic mobility shift assay the DNA construct

CC was found to bind IL-4 and IL-13 moderately.  
 XX  
 SQ Sequence 19 BP; 4 A; 5 C; 4 G; 6 T; 0 other;

Query Match 100.0%; Score 9; DB 17; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
 |||||  
 Db 16 TTCTGAGAA 8

```

RESULT 15
AAV56941/C
ID AAV56941 standard; DNA; 19 BP.
XX
AC AAV56941;
XX
DT 02-DEC-1998 (first entry)
XX
DE Regulatory element containing oligonucleotide #100.
XX
KM Cytokine-responsive regulatory; primer; promoter; detection; isolation;
transcriptional control; STAT protein; screening; agonist; ss.
XX
OS Synthetic.
XX
PN US5814517-A.
XX
PD 29-SEP-1998.
XX
PF 27-MAR-1995; 95US-0410779.
XX
PR 27-MAR-1995; 95US-0410779.
PR 14-APR-1994; 94US-0228935.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Lamb 1P, Seidel HM;
XX
DR WPI: 1998-541763/46.
XX
PT DNA constructs containing cytokine-responsive regulatory elements -
PT useful in assays for transcription-regulating proteins or gene
transcription agonists or antagonists
XX
PS Example 1: Column 19-20; 58pp; English.
XX
CC AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
CC production of constructs comprising a cytokine-responsive regulatory
CC element linked to a promoter which is linked to a heterologous coding
CC sequence so that the coding sequence is under the transcriptional
CC control of the regulatory element and the promoter, where the regulatory
CC element has a nucleotide sequence selected from TTCNCGAA, TTAANYTA, and
CC TTGAYTAA where N is A, T, C or G, and Y = 3 or 4. The constructs can be
CC used to detect or isolate transcription-regulating proteins, e.g. STAT
CC proteins, in a sample by contacting the sample with the construct so that
CC the protein binds to the regulatory element, and detecting or separating
CC the resulting complex. The cells can be used in screening assays for
CC agonists of gene transcription, in which the level of expression of the
CC coding sequence is measured in the presence and absence of a test
CC compound or in the presence of the corresponding cytokine.
XX
SQ Sequence 19 BP; 4 A; 5 C; 4 G; 6 T; 0 other;

Query Match 100.0%; Score 9; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9
   |||||
Db 16 TTCTGAGAA 8

```

Search completed: August 20, 2002, 23:27:54  
 Job time: 3670 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 22:19:24 ; Search time 43.04 Seconds  
(without alignments)  
51.364 Million cell updates/sec

Title: NA\_SEQ  
Perfect score: 9  
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 403436

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/pdata2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/pdata2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/pdata2/ina/5A\_COMB.seq:\*  
4: /cgn2\_6/pdata2/ina/5B\_COMB.seq:\*  
5: /cgn2\_6/pdata2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/pdata2/ina/beckfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	9	1 US-08-411-020-13	Sequence 13, Appl
2	9	100.0	9	1 US-08-369-796-34	Sequence 34, Appl
3	9	100.0	9	1 US-08-410-779B-35	Sequence 35, Appl
4	9	100.0	9	2 US-08-852-091-34	Sequence 34, Appl
5	9	100.0	9	5 PCT-US95-04477-35	Sequence 35, Appl
6	9	100.0	9	5 PCT-US95-17025-34	Sequence 34, Appl
7	9	100.0	15	2 US-08-585-684B-1819	Sequence 1819, Ap
8	9	100.0	15	2 US-08-585-684B-1820	Sequence 1820, Ap
9	9	100.0	15	4 US-09-038-073-1819	Sequence 1819, Ap
10	9	100.0	15	4 US-09-038-073-1820	Sequence 1820, Ap
11	9	100.0	19	1 US-08-411-020-56	Sequence 56, Appl
12	9	100.0	19	1 US-08-411-020-57	Sequence 57, Appl
13	9	100.0	19	1 US-08-410-779B-100	Sequence 100, Appl
14	9	100.0	19	1 US-08-410-779B-101	Sequence 101, Appl
15	9	100.0	19	5 PCT-US95-04477-100	Sequence 100, App
16	9	100.0	19	5 PCT-US95-04477-101	Sequence 101, App
17	9	100.0	20	2 US-08-723-415B-21	Sequence 21, Appl
18	9	100.0	20	3 US-09-078-317-7	Sequence 7, Appl1
19	9	100.0	20	3 US-08-600-882-20	Sequence 20, Appl
20	9	100.0	20	3 US-09-189-627A-21	Sequence 21, Appl
21	9	100.0	20	5 PCT-US94-10261A-20	Sequence 20, Appl
22	9	100.0	22	1 US-08-198-431-18	Sequence 18, Appl
23	9	100.0	22	1 US-08-564-955-18	Sequence 18, Appl
24	9	100.0	22	2 US-08-537-874-18	Sequence 18, Appl
25	9	100.0	22	3 US-08-929-140-13	Sequence 13, Appl
26	9	100.0	22	3 US-08-621-859-18	Sequence 18, Appl
27	9	100.0	22	3 US-09-100-856A-18	Sequence 18, Appl

28	9	100.0	22	4 US-09-075-511-18	Sequence 18, Appl
29	9	100.0	22	4 US-09-099-015-18	Sequence 18, Appl
30	9	100.0	22	4 US-09-232-863-18	Sequence 13, Appl
31	9	100.0	22	4 US-09-560-579A-13	Sequence 13, Appl
32	9	100.0	22	4 US-09-133-508A-18	Sequence 18, Appl
33	9	100.0	22	4 US-09-165-060-18	Sequence 18, Appl
34	9	100.0	22	4 US-09-501-698-18	Sequence 18, Appl
35	9	100.0	22	4 US-09-590-778-18	Sequence 18, Appl
36	9	100.0	23	3 US-09-067-284-2	Sequence 2, Appl1
37	9	100.0	24	2 US-08-953-041-4	Sequence 4, Appl1
38	9	100.0	24	4 US-09-159-417-4	Sequence 4, Appl1
39	9	100.0	25	3 US-08-781-891-39	Sequence 39, Appl
40	9	100.0	25	3 US-08-781-891-141	Sequence 141, App
41	9	100.0	25	3 US-08-912-272-70	Sequence 70, Appl
42	9	100.0	25	4 US-09-026-039-70	Sequence 70, Appl
43	9	100.0	26	1 US-08-379-078-553	Sequence 553, App
44	9	100.0	26	1 US-08-379-078-558	Sequence 558, App
45	9	100.0	26	1 US-08-379-078-663	Sequence 663, App

## ALIGNMENTS

RESULT 1  
US-08-411-020-13/c  
Sequence 13, Application US/08411020  
Patent No. 5712094  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, H. MARTI  
APPLICANT: LAMB, I. PETER  
TITLE OF INVENTION: CHAN, SHIN-SHAY TIAN  
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ligand Pharmaceuticals Incorporated  
STREET: 9393 Towne Centre Drive  
City: San Diego  
STATE: California  
COUNTRY: US  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/411,020  
FILING DATE: 27-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jurgensen, Thomas E.  
REGISTRATION NUMBER: 34,195  
REFERENCE/DOCKET NUMBER: 016-0030.US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 550-7675  
TELEFAX: (619) 535-3906  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
SYNTHETIC DNA"  
US-08-411-020-13

Query Match 100.0% Score 9; DB 1; Length 9;  
Best Local Similarity 100.0% Pred. No. 2.5e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 tctctgagaa 9
      |||
      9 TTCTGAGAA 1

RESULT 2
US-08-369-796-34/C
; Sequence 34, Application US/08369796
; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA synthetic probe
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-369-796-34

Query Match 100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctctgagaa 9
      |||
      9 TTCTGAGAA 1

RESULT 3
US-08-410-779B-35/C
; Sequence 35, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
STREET: 9393 TOWNE CENTRE DRIVE
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
US-08-410-779B-35

Query Match 100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctctgagaa 9
      |||
      9 TTCTGAGAA 1

RESULT 4
US-08-852-091-34/C
; Sequence 34, Application US/08852091
; Patent No. 5863228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
```

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/369,796  
FILING DATE: 06-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA synthetic probe  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-852-091-34

Query Match 100.0%; Score 9; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
|||||  
Db 9 TTCTGAGAA 1

RESULT 5  
PCT-US95-04477-35/c  
Sequence 35, Application PC/TUS9504477  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO  
TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 165  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04477  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/228,935  
FILING DATE: 14-APR-1994  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
SYNTHETIC DNA"  
PCT-US95-04477-35

Query Match 100.0%; Score 9; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
|||||  
Db 9 TTCTGAGAA 1

RESULT 6  
PCT-US95-17025-34/c  
Sequence 34, Application PC/TUS9517025  
GENERAL INFORMATION:  
APPLICANT: James E. Darnell, Jr.  
APPLICANT: Zilong Wen  
APPLICANT: Curt M. Horvath  
APPLICANT: Zhong Zhong  
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
City: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17025  
FILING DATE: 28-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/369,796  
FILING DATE: 06-JAN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA synthetic probe  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US95-17025-34

Query Match 100.0%; Score 9; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
|||||  
Db 9 TTCTGAGAA 1

RESULT 7  
US-08-585-684B-1819/c  
Sequence 1819, Application US/08585684B  
Patent No. 5877021  
GENERAL INFORMATION:  
APPLICANT: Slinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751

```

CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1819:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-1819

Query Match      100.0%; Score 9; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. NO. 9.9e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ttctgagaa 9
    |||||
Db 15 TTCTGAGAA 7

RESULT 8
US-08-585-684B-1820/c
Sequence 1820, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: MCSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
NUMBER OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
CORRESPONDENCE ADDRESSES:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1819:
SEQUENCE CHARACTERISTICS:
```

```

APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1820:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-1820

Query Match      100.0%; Score 9; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. NO. 9.9e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ttctgagaa 9
    |||||
Db 12 TTCTGAGAA 4

RESULT 9
US-09-038-073-1819/c
Sequence 1819, Application US/09038073
Patent No. 6194150
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: MCSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
NUMBER OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
CORRESPONDENCE ADDRESSES:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1819:
SEQUENCE CHARACTERISTICS:
```

LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-038-073-1819

Query Match 100.0%; Score 9; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
|||||  
Db 15 TTCTGAGA 7

RESULT 10  
US-09-038-073-1820/C  
Sequence 1820, Application US/09038073  
Patent No. 6194150

GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,073  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,684

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1820:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-038-073-1820

Query Match 100.0%; Score 9; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
|||||  
Db 12 TTCTGAGA 4

RESULT 11  
US-08-411-020-56/C  
Sequence 56, Application US/08411020  
Patent No. 5712094

GENERAL INFORMATION:  
APPLICANT: SEIDEL, H. MARTI  
APPLICANT: LAMB, I. PETER  
APPLICANT: CHAN, SHIN-SHAY TIAN  
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR  
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ligand Pharmaceuticals Incorporated  
STREET: 9393 Towne Centre Drive  
CITY: San Diego  
STATE: California  
COUNTRY: US  
ZIP: 92121

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/411,020  
FILING DATE: 27-MAR-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Jurgensen, Thomas E.  
REGISTRATION NUMBER: 34,195  
REFERENCE/DOCKET NUMBER: 016-0030.US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 550-7675  
TELEFAX: (619) 535-3906

INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
SYNTHETIC DNA"

US-08-411-020-56  
Query Match 100.0%; Score 9; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
|||||  
Db 16 TTCTGAGA 8

RESULT 12  
US-08-411-020-57  
Sequence 57, Application US/08411020  
Patent No. 5712094

GENERAL INFORMATION:  
APPLICANT: SEIDEL, H. MARTI  
APPLICANT: LAMB, I. PETER  
APPLICANT: CHAN, SHIN-SHAY TIAN  
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR  
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ligand Pharmaceuticals Incorporated  
STREET: 9393 Towne Centre Drive  
CITY: San Diego  
STATE: California  
COUNTRY: US

US-08-411-020-57  
Query Match 100.0%; Score 9; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,020
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jurgensen, Thomas E.
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0030.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; SYNTHETIC DNA"
US-08-411-020-57
```

```
Query Match          100.0%; Score 9; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 tctctgagaa 9
    |||
DB 8 TTCTGAGAA 16
```

```
RESULT 13
US-08-410-779B-100/C
; Sequence 100, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
; STREET: 9393 TOWNE CENTRE DRIVE
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
```

```
TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; SYNTHETIC DNA"
US-08-410-779B-100
```

```
Query Match          100.0%; Score 9; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 tctctgagaa 9
    |||
DB 16 TTCTGAGAA 8
```

```
RESULT 14
US-08-410-779B-101
; Sequence 101, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
; STREET: 9393 TOWNE CENTRE DRIVE
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; SYNTHETIC DNA"
US-08-410-779B-101
```

```
Query Match          100.0%; Score 9; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 ttctgagaa 9  
|||||  
Db 8 TTCTGAGAA 16

RESULT 15  
PCT-US95-04477-100/c  
; Sequence 100, Application PC/TUS9504477  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO  
; TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 165  
; COMPUTER-READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04477  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/228,935  
; FILING DATE: 14-APR-1994  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
; DESCRIPTION: SYNTHETIC DNA"  
; PCT-US95-04477-100

Query Match 100.0%; Score 9; DB 5; Length 19;  
Best local Similarity 100.0%; Pred. No. 1e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgagaa 9  
|||||  
Db 16 TTCTGAGAA 8

Search completed: August 20, 2002, 23:24:06  
Job time: 3882 sec

**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 21:26:14 ; Search time 1559.67 Seconds  
(without alignments)  
77.884 Million cell updates/sec

Title: NA\_SEQ  
Perfect score: 9  
Sequence: 1 tctcgaga 9

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

28088

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estrov:\*  
6: em\_estrpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	29	12	AZ818898
2	8	88.9	29	12	AZ313531
3	8	88.9	20	12	AZ303578
4	8	88.9	24	12	AZ819888
5	8	88.9	26	12	AZ313876
6	8	88.9	27	12	AZ387860
7	8	88.9	28	12	AZ648296
8	8	88.9	30	12	AZ514561
9	8	82.2	19	12	AZ399220
10	7	82.2	19	12	AZ810627
11	7	82.2	19	12	AZ835621
12	7	82.2	20	12	AZ468141
13	7	82.2	21	12	AZ360212
14	7	82.2	22	12	AZ30664
15	7	82.2	22	12	AZ457101
16	7	82.2	22	12	TA196602P
17	7	82.2	23	12	AZ388663

18	7	82.2	23	12	AZ424145
19	7	82.2	24	12	AZ343358
20	7	82.2	24	12	AZ357286
21	7	82.2	24	12	AZ446127
22	7	82.2	24	12	AZ595959
23	7	82.2	24	12	AZ596086
24	7	82.2	24	12	TA196H02P
25	7	82.2	25	10	D1996
26	7	82.2	26	12	AZ514399
27	7	82.2	26	12	AZ602086
28	7	82.2	27	12	AZ778941
29	7	82.2	28	9	AU012291
30	7	82.2	28	12	AZ346840
31	7	82.2	28	12	AZ609297
32	7	82.2	28	12	TA108B080
33	7	82.2	29	12	AZ818898
34	7	82.2	29	12	AZ852213
35	7	82.2	30	12	AZ510129
36	7	77.8	19	12	AZ473867
37	7	77.8	19	12	AZ489350
38	7	77.8	20	12	AZ489135
39	7	77.8	20	12	AZ780925
40	7	77.8	20	12	AZ782243
41	7	77.8	20	12	AZ626828
42	7	77.8	21	12	AZ488178
43	7	77.8	21	12	AZ595078
44	7	77.8	21	12	AZ806440
45	7	77.8	22	9	AI224088

#### ALIGNMENTS

RESULT 1  
LOCUS AZ818898 29 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0089N1F Mouse 10kb plasmid UGCCIM library Mus musculus genomic  
clone UGCC2M0089N1 F, DNA sequence.  
ACCESSION AZ818898  
VERSION AZ818898.1 GI:12988806  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.  
1 (bases 1 to 29)  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0089 row: N column: 11  
Seq primer: CGTTGTAAACGACGCCAAGT  
Class: plasmid ends  
High quality sequence stop: 29.  
Location/Qualifiers  
1..29  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGGC2M0089N1F"  
/clone\_lib="Mouse 10kb plasmid UGCCIM library"

#### FEATURES

source

/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g11473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 12 a 8 c 4 g 5 t  
ORIGIN

Query Match 100.0%; Score 9; DB 12; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.8e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
|||||  
Db 9 TTCTGAGAA 17

RESULT 2  
LOCUS A2313531 19 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0029N07 Mouse 10kb plasmid U08C1M library Mus musculus genomic  
clone U08C1M0029N07 R, DNA sequence.  
ACCESSION A2313531  
VERSION A2313531.1 GI:10358522  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0029 row: N column: 07  
Seq primer: CACACAGCAACACCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U08C1M0029N07"

/clone\_11b="Mouse 10kb plasmid U08C1M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g11473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 6 a 2 c 5 g 6 t  
ORIGIN

Query Match 88.9%; Score 8; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 tctgagaa 9  
|||||  
Db 8 TCTGAGAA 15

RESULT 3  
LOCUS A2303578 20 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0003H07F Mouse 10kb plasmid U08C1M library Mus musculus genomic  
clone U08C1M0003H07 F, DNA sequence.  
ACCESSION A2303578  
VERSION A2303578.1 GI:10338956  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0003 row: H column: 07  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1. .20  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

FEATURES  
source  
1. .19  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U08C1M0029N07"

/clone="UUGC1M003H07"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1147321141gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
ORIGIN  
8 a 2 c 3 g 7 t

Query Match  
Best Local Similarity 100.0%; Score 8; DB 12; Length 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 tctgaga 9  
|||||||  
Db 10 TCTGAGA 17

RESULT 4  
LOCUS AZ819888 24 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0091H18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0091H18 R, DNA sequence.  
ACCESSION AZ819888  
VERSION AZ819888.1 GI:12989796  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 24)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0091 row: H column: 18  
Seq primer: CACACAGGAACACGACATACAC  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
1. 24  
/organism="Mus musculus"  
/strain="C57BL/6J"

/db\_xref="taxon:10090"  
/clone="UUGC2M0091H18"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1147321141gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
ORIGIN  
6 a 5 c 5 g 8 t

Query Match  
Best Local Similarity 100.0%; Score 8; DB 12; Length 24;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctgaga 8  
|||||||  
Db 14 TTCTGAGA 21

RESULT 5  
LOCUS AZ313876 26 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0030H21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0030H21 F, DNA sequence.  
ACCESSION AZ313876  
VERSION AZ313876.1 GI:10359208  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0030 row: H column: 21  
Seq primer: CCGTGAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers  
1. 26  
/organism="Mus musculus"

```
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="UUGC1M0030H21"  
/clone_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g114732114[g1AF129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."
```

BASE COUNT 6 a 6 c 9 g 5 t  
ORIGIN

Query Match 88.9%; Score 8; DB 12; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.9e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctgtaga 8  
|||||||  
Db 8 TCTGTAGA 1

RESULT 6  
LOCUS A2387860 27 bp DNA linear GSS 02-OCT-2000  
DEFINITION IM0147M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0147M20 R, DNA sequence.  
ACCESSION A2387860  
VERSION A2387860.1 GI:10501568  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0147 row: M column: 20  
Seq primer: CACACAGCAACACCTATGACG  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers 1..27

FEATURES  
Source

```
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="UUGC1M0147M20"  
/clone_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g114732114[g1AF129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."
```

BASE COUNT 8 a 3 c 7 g 9 t  
ORIGIN

Query Match 88.9%; Score 8; DB 12; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.9e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 tctgtaga 9  
|||||||  
Db 4 TCTGTAGA 11

RESULT 7  
LOCUS A2648296 28 bp DNA linear GSS 14-DEC-2000  
DEFINITION IM0517E15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0517E15 F, DNA sequence.  
ACCESSION A2648296  
VERSION A2648296.1 GI:11780621  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0517 row: E column: 15  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 28.  
Location/Qualifiers

FEATURES

```
source
1. 28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0517E15"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g11473211419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT 11 a 7 c 4 g 6 t

ORIGIN

Query Match 88.9%; Score 8; DB 12; Length 28;  
Best Local Similarity 100.0%; Pred. No. 2.9e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 tctcgagaa 9  
|||||||  
Db 17 TCTGAGAA 24

RESULT 8  
A2514561 30 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0361N07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0361N07 F, DNA sequence.  
ACCESSION A2514561  
VERSION A2514561.1 GI:10695793  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 30)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0361 row: N column: 07  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 30.

JOURNAL  
COMMENT

FEATURES

source

Location/Qualifiers

1. 30  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0361N07"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/notes="Vector: PMD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g11473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 13 a 2 c 10 g 5 t

ORIGIN

Query Match 88.9%; Score 8; DB 12; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.9e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 tctcgagaa 9  
|||||||  
Db 3 TCTGAGAA 10

RESULT 9  
A2399220 19 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0164P23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0164P23 R, DNA sequence.  
ACCESSION A2399220  
VERSION A2399220.1 GI:10514292  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0164 row: P column: 23  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends

JOURNAL  
COMMENT

High quality sequence stop: 19.

FEATURES  
Location/Qualifiers

source

```
1..19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C2M0164P23"
/clone_11b="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g114732114[gblAF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT  
ORIGIN

```
4 a 2 c 4 g 9 t
```

Query Match 82.2%; Score 7.4; DB 12; Length 19;

Best Local Similarity 88.9%; Pred. No. 7.2e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctctgaga 9

DB 6 TTCTGAGTA 14

RESULT 10  
LOCUS

DEFINITION A2810627 19 bp DNA linear GSS 20-FEB-2001

ACCESSION 2M0076H17F Mouse 10kb plasmid U08C1M library Mus musculus genomic

VERSION A2810627

KEYWORDS A2810627.1 GI:12978066

SOURCE GSS.

ORGANISM house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0076 row: H column: 17

Seq primer: CGTTGTAACGACGCCACG

Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
Location/Qualifiers

source

```
1..19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C2M0076H17"
/clone_11b="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g114732114[gblAF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT  
ORIGIN

```
6 a 5 c 1 g 7 t
```

Query Match 82.2%; Score 7.4; DB 12; Length 19;

Best Local Similarity 88.9%; Pred. No. 7.2e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctctgaga 9

DB 15 TTATGAGAA 7

RESULT 11

LOCUS

DEFINITION A2835621 19 bp DNA linear GSS 20-FEB-2001

ACCESSION 2M0129J2R Mouse 10kb plasmid U08C1M library Mus musculus genomic

VERSION A2835621

KEYWORDS A2835621.1 GI:13005529

SOURCE GSS.

ORGANISM house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0129 row: L column: 21

Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

## FEATURES

source

1..19  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0129L21"  
 /clone.lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

6 a 3 c 3 g 7 t

## ORIGIN

Query Match 82.2%; Score 7.4; DB 12; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 7.2e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
 |||||  
 Db 2 TTCTGTGAA 10

## RESULT 12

A2468141

LOCUS A2468141 20 bp DNA linear GSS 04-OCT-2000  
 DEFINITION 1M0281D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0281D04 F, DNA sequence.

ACCESSION A2468141  
 VERSION A2468141.1 GI:10626266  
 KEYWORDS GSS.

SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00

## JOURNAL COMMENT

Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00

Plate: 0281 Row: D Column: 04  
 Seq primer: CATTGTAAACGACGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

## FEATURES

source

1..20  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0281D04"  
 /clone.lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

7 a 0 c 4 g 9 t

## ORIGIN

Query Match 82.2%; Score 7.4; DB 12; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 7.2e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
 |||||  
 Db 7 TTATGAGAA 15

## RESULT 13

A2360212

LOCUS A2360212 21 bp DNA linear GSS 02-OCT-2000  
 DEFINITION 1M0103K04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0103K04 F, DNA sequence.

ACCESSION A2360212  
 VERSION A2360212.1 GI:10473912  
 KEYWORDS GSS.

SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu

Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu

## JOURNAL COMMENT

Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0103 row: K column: 04  
 Seq primer: CGTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers

## FEATURES

source

```

1..21
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUCG1M0103K04"
    /clone_lib="Mouse 10kb plasmid UUCG1M library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /note="Vector: PMD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PMD42 (911473211419b|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
BASE COUNT      6 a          7 c          5 g          3 t
ORIGIN

```

Query Match 82.2%; Score 7.4; DB 12; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 7.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ttctagaa 9  
 ||||| 111  
 Db 7 TTCTGGAA 15

## RESULT 14

AZ430664 22 bp DNA linear GSS 03-OCT-2000  
 LOCUS IM0215D17F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 DEFINITION clone UUCG1M0215D17 F, DNA sequence.

ACCESSION AZ430664  
 VERSION AZ430664.1 GI:10554677  
 KEYWORDS GSS.

SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## JOURNAL COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0215 row: D column: 17  
 Seq primer: CGTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 22.  
 Location/Qualifiers

## FEATURES

source

```

1..22
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUCG1M0215D17"
    /clone_lib="Mouse 10kb plasmid UUCG1M library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /note="Vector: PMD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PMD42 (911473211419b|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
BASE COUNT      6 a          4 c          3 g          9 t
ORIGIN

```

Query Match 82.2%; Score 7.4; DB 12; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 7.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ttctagaa 9  
 ||||| 111  
 Db 13 TTCTGGAA 21

## RESULT 15

AZ457101 22 bp DNA linear GSS 04-OCT-2000  
 LOCUS IM0260J17F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 DEFINITION clone UUCG1M0260J17 F, DNA sequence.

ACCESSION AZ457101  
 VERSION AZ457101.1 GI:10615226  
 KEYWORDS GSS.

SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## JOURNAL COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606



Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0260 row: j column: 17  
 Seq primer: CGTGTAAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 22.

# FEATURES

Location/Qualifiers  
 1..22  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U06C1M0260U17"  
 /clone\_1lb="Mouse 10kb plasmid U06C1M library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, F'-resistant, F-"  
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi14732114|gb|AF128072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 8 c 2 g 6 t  
 ORIGIN

Query Match 82.2%; Score 7.4; DB 12; Length 22;

Best Local Similarity 88.9%; Pred. No. 7.3e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ttctgagaa 9  
 || |||||  
 Db 15 TTTTGAGAA 7

Search completed: August 20, 2002, 22:51:42  
 Job time: 5128 sec

THIS PAGE BLANK (USPTO)